

Search for

Limits Preview/Index History Clipboard Details

Display Show Send to Hide: ☐ sequence ☐ all but gene, CDS and mRNA

Range: from to ☐ Reverse complemented strand Features:

[1: AJ242651](#). Reports Hepatitis C virus...[gi:5441831]

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LOCUS AJ242651 8637 bp RNA linear SYN 11-MAY-2000

DEFINITION Hepatitis C virus replicon I377/NS2-3'UTR.

ACCESSION AJ242651

VERSION AJ242651.1 GI:5441831

KEYWORDS core-neo gene; NS2 gene; NS2 proteinase; NS3 gene; NS3 proteinase/helicase; NS3/4A proteinase cofactor; NS4A gene; NS4B gene; NS4b protein; NS5a gene; NS5A phosphoprotein; NS5b gene; NS5B RNA dependant RNA polymerase; polyprotein.

SOURCE Hepatitis C virus replicon I377/NS2-3'UTR

ORGANISM Hepatitis C virus replicon I377/NS2-3'UTR
other sequences; artificial sequences; vectors.

REFERENCE 1

AUTHORS Lohmann,V., Korner,F., Koch,J., Herian,U., Theilmann,L. and Bartenschlager,R.

TITLE Replication of subgenomic hepatitis C virus RNAs in a hepatoma cell line

JOURNAL Science 285 (5424), 110-113 (1999)

PUBMED 10390360

REFERENCE 2 (bases 1 to 8637)

AUTHORS Bartenschlager,R.

TITLE Direct Submission

JOURNAL Submitted (26-MAY-1999) Bartenschlager R., Institute for Virology, Johannes Gutenberg - University Mainz, Obere Zahlbacher Strasse 67, 55131 Mainz, GERMANY

FEATURES

source Location/Qualifiers

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Aug 28 2007 16:53:42



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.17 [Aug-26-2007]

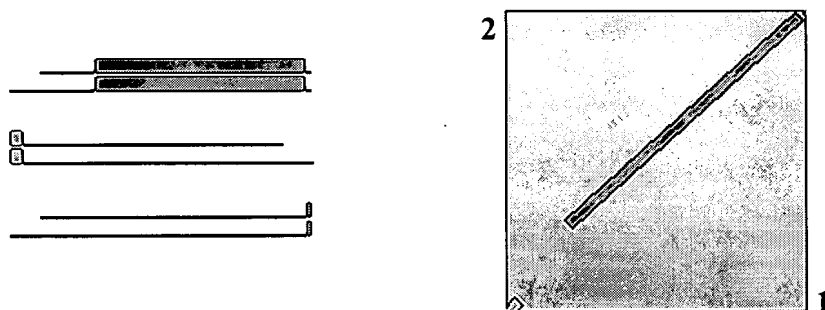
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☐ Show CDS translation

Sequence 1: [gi|5441831|Hepatitis C virus replicon I377/NS2-3'UTR](#)

Length = 8636 (1 .. 8637)

Sequence 2: [gi|5420376|Hepatitis C virus type 1b complete genome, isolate Con1](#)

Length = 9605 (1 .. 9605)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.



Score = 1.261e+04 bits (6560), Expect = 0.0
 Identities = 6646/6646 (100%), Gaps = 0/6646 (0%)
 Strand=Plus/Plus

Query	1799	CCATGGACCGGGAGATGGCAGCATCGTGCGGAGGCGCGGTTTTTCGTAGGTCTGATACTCT	1858
Sbjct	2767	CCATGGACCGGGAGATGGCAGCATCGTGCGGAGGCGCGGTTTTTCGTAGGTCTGATACTCT	2826
Query	1859	TGACCTTGTCACCGCACTATAAGCTGTTCTCGCTAGGCTCATATGGTGGTTACAATATT	1918
Sbjct	2827	TGACCTTGTCACCGCACTATAAGCTGTTCTCGCTAGGCTCATATGGTGGTTACAATATT	2886
Query	1919	TTATCACCAGGGCCGAGGCACACTTGCAAGTGTGGATCCCCCCCCCTCAACGTTTCGGGGGG	1978

Sbjct	2887	TTATCACCAGGGCCGAGGCACACTTGCAAGTGTGGATCCCCCCCCTCAACGTTTCGGGGGG	2946
Query	1979	GCCGCGATGCCGTCATCCTCCTCACGTGCGCGATCCACCCAGAGCTAATCTTTACCATCA	2038
Sbjct	2947	GCCGCGATGCCGTCATCCTCCTCACGTGCGCGATCCACCCAGAGCTAATCTTTACCATCA	3006
Query	2039	CCAAAATCTTGCTCGCCATACTCGGTCCACTCATGGTGCTCCAGGCTGGTATAACCAAAG	2098
Sbjct	3007	CCAAAATCTTGCTCGCCATACTCGGTCCACTCATGGTGCTCCAGGCTGGTATAACCAAAG	3066
Query	2099	TGCCGTACTTCGTGCGCGCACACGGGGCTCATTCGTGCATGCATGCTGGTGCGGAAGGTTG	2158
Sbjct	3067	TGCCGTACTTCGTGCGCGCACACGGGGCTCATTCGTGCATGCATGCTGGTGCGGAAGGTTG	3126
Query	2159	CTGGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACG	2218
Sbjct	3127	CTGGGGGTCAATTATGTCCAAATGGCTCTCATGAAGTTGGCCGCACTGACAGGTACGTACG	3186
Query	2219	TTTATGACCATCTCACCCCACTGCGGGACTGGGCCCACGCGGGCCTACGAGACCTTGCGG	2278
Sbjct	3187	TTTATGACCATCTCACCCCACTGCGGGACTGGGCCCACGCGGGCCTACGAGACCTTGCGG	3246
Query	2279	TGGCAGTTGAGCCCGTCGTCTTCTCTGATATGGAGACCAAGGTTATCACCTGGGGGGCAG	2338
Sbjct	3247	TGGCAGTTGAGCCCGTCGTCTTCTCTGATATGGAGACCAAGGTTATCACCTGGGGGGCAG	3306
Query	2339	ACACCGCGGCGTGTGGGGACATCATCTTGGGCCTGCCCCTCTCCGCCCGCAGGGGGAGGG	2398
Sbjct	3307	ACACCGCGGCGTGTGGGGACATCATCTTGGGCCTGCCCCTCTCCGCCCGCAGGGGGAGGG	3366
Query	2399	AGATACATCTGGGACCGGCAGACAGCCTTGAAGGGCAGGGGTGGCGACTCCTCGCGCCTA	2458
Sbjct	3367	AGATACATCTGGGACCGGCAGACAGCCTTGAAGGGCAGGGGTGGCGACTCCTCGCGCCTA	3426
Query	2459	TTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCACTAGCCTCACAG	2518
Sbjct	3427	TTACGGCCTACTCCCAACAGACGCGAGGCCTACTTGGCTGCATCATCACTAGCCTCACAG	3486
Query	2519	GCCGGGACAGGAACCAGGTCGAGGGGGAGGTCCAAGTGGTCTCCACCGCAACACAATCTT	2578
Sbjct	3487	GCCGGGACAGGAACCAGGTCGAGGGGGAGGTCCAAGTGGTCTCCACCGCAACACAATCTT	3546
Query	2579	TCCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGGTGCCGGCTCAAAGA	2638
Sbjct	3547	TCCTGGCGACCTGCGTCAATGGCGTGTGTTGGACTGTCTATCATGGTGCCGGCTCAAAGA	3606
Query	2639	CCCTTGCCGGCCCCAAAGGGCCCCAATCACCCAAATGTACACCAATGTGGACCAGGACCTCG	2698
Sbjct	3607	CCCTTGCCGGCCCCAAAGGGCCCCAATCACCCAAATGTACACCAATGTGGACCAGGACCTCG	3666
Query	2699	TCGGCTGGCAAGCGCCCCCGGGGCGCGTTCTTGACACCATGCACCTGCGGCAGCTCGG	2758
Sbjct	3667	TCGGCTGGCAAGCGCCCCCGGGGCGCGTTCTTGACACCATGCACCTGCGGCAGCTCGG	3726
Query	2759	ACCTTTACTTGGTCACGAGGCATGCCGATGTCAATTCGGTGCGCCGGCGGGGCGACAGCA	2818
Sbjct	3727	ACCTTTACTTGGTCACGAGGCATGCCGATGTCAATTCGGTGCGCCGGCGGGGCGACAGCA	3786
Query	2819	GGGGGAGCCTACTCTCCCCAGGCCCGTCTCCTACTTGAAGGGCTCTTCGGGCGGTCCAC	2878

Sbjct	3787	GGGGGAGCCTACTCTCCCCCAGGCCCGTCTCTACTTGAAGGGCTCTTCGGGCGGTCCAC	3846
Query	2879	TGCTCTGCCCCCTCGGGGCACGCTGTGGGCATCTTTCGGGCTGCCGTGTGCACCCGAGGGG	2938
Sbjct	3847	TGCTCTGCCCCCTCGGGGCACGCTGTGGGCATCTTTCGGGCTGCCGTGTGCACCCGAGGGG	3906
Query	2939	TTGCGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCCGG	2998
Sbjct	3907	TTGCGAAGGCGGTGGACTTTGTACCCGTCGAGTCTATGGAAACCACTATGCGGTCCCCGG	3966
Query	2999	TCTTCACGGACAACCTCGTCCCTCCGGCCGTACCGCAGACATTCCAGGTGGCCCATCTAC	3058
Sbjct	3967	TCTTCACGGACAACCTCGTCCCTCCGGCCGTACCGCAGACATTCCAGGTGGCCCATCTAC	4026
Query	3059	ACGCCCCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGGT	3118
Sbjct	4027	ACGCCCCCTACTGGTAGCGGCAAGAGCACTAAGGTGCCGGCTGCGTATGCAGCCCAAGGGT	4086
Query	3119	ATAAGGTGCTTGTCTGAACCCGTCGTCGCCGCCACCCTAGGTTTCGGGGCGTATATGT	3178
Sbjct	4087	ATAAGGTGCTTGTCTGAACCCGTCGTCGCCGCCACCCTAGGTTTCGGGGCGTATATGT	4146
Query	3179	CTAAGGCACATGGTATCGACCCTAACATCAGAACCGGGGTAAGGACCATCACCACGGGTG	3238
Sbjct	4147	CTAAGGCACATGGTATCGACCCTAACATCAGAACCGGGGTAAGGACCATCACCACGGGTG	4206
Query	3239	CCCCCATCACGTACTCCACCTATGGCAAGTTTCTTGCCGACGGTGGTTGCTCTGGGGGCG	3298
Sbjct	4207	CCCCCATCACGTACTCCACCTATGGCAAGTTTCTTGCCGACGGTGGTTGCTCTGGGGGCG	4266
Query	3299	CCTATGACATCATAATATGTGATGAGTGCCACTCAACTGACTCGACCACTATCCTGGGCA	3358
Sbjct	4267	CCTATGACATCATAATATGTGATGAGTGCCACTCAACTGACTCGACCACTATCCTGGGCA	4326
Query	3359	TCGGCAGTCTGGACCAAGCGGAGACGGCTGGAGCGCGACTCGTCGTGCTCGCCACCG	3418
Sbjct	4327	TCGGCAGTCTGGACCAAGCGGAGACGGCTGGAGCGCGACTCGTCGTGCTCGCCACCG	4386
Query	3419	CTACGCCTCCGGGATCGGTACCGTGCCACATCCAAACATCGAGGAGGTGGCTCTGTCCA	3478
Sbjct	4387	CTACGCCTCCGGGATCGGTACCGTGCCACATCCAAACATCGAGGAGGTGGCTCTGTCCA	4446
Query	3479	GCACTGGAGAAATCCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATCAAGGGGGGGA	3538
Sbjct	4447	GCACTGGAGAAATCCCCTTTTATGGCAAAGCCATCCCCATCGAGACCATCAAGGGGGGGA	4506
Query	3539	GGCACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTGTCCG	3598
Sbjct	4507	GGCACCTCATTTTCTGCCATTCCAAGAAGAAATGTGATGAGCTCGCCGCGAAGCTGTCCG	4566
Query	3599	GCCTCGGACTCAATGCTGTAGCATATTACCGGGGCCTTGATGTATCCGTCATACCAACTA	3658
Sbjct	4567	GCCTCGGACTCAATGCTGTAGCATATTACCGGGGCCTTGATGTATCCGTCATACCAACTA	4626
Query	3659	GCGGAGACGTCATTGTCTGTAGCAACGGACGCTCTAATGACGGGCTTTACCGGCGATTTTCG	3718
Sbjct	4627	GCGGAGACGTCATTGTCTGTAGCAACGGACGCTCTAATGACGGGCTTTACCGGCGATTTTCG	4686
Query	3719	ACTCAGTGATCGACTGCAATACATGTGTCAACCAGACAGTCGACTTCAGCCTGGACCCGA	3778

Sbjct	4687	ACTCAGTGATCGACTGCAATACATGTGTACCCAGACAGTCGACTTCAGCCTGGACCCGA	4746
Query	3779	CCTTCACCATTGAGACGACGACCGTGCCACAAGACGCGGTGTACGCTCGCAGCGGCGAG	3838
Sbjct	4747	CCTTCACCATTGAGACGACGACCGTGCCACAAGACGCGGTGTACGCTCGCAGCGGCGAG	4806
Query	3839	GCAGGACTGGTAGGGGCAGGATGGGCATTTACAGGTTTGTGACTCCAGGAGAACGGCCCT	3898
Sbjct	4807	GCAGGACTGGTAGGGGCAGGATGGGCATTTACAGGTTTGTGACTCCAGGAGAACGGCCCT	4866
Query	3899	CGGGCATGTTCGATTTCCTCGGTTCTGTGCGAGTGCTATGACGCGGGCTGTGCTTGGTACG	3958
Sbjct	4867	CGGGCATGTTCGATTTCCTCGGTTCTGTGCGAGTGCTATGACGCGGGCTGTGCTTGGTACG	4926
Query	3959	AGCTCACGCCCCGCCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACACCAGGGTTGC	4018
Sbjct	4927	AGCTCACGCCCCGCCGAGACCTCAGTTAGGTTGCGGGCTTACCTAAACACACCAGGGTTGC	4986
Query	4019	CCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCCTCACCCACATAG	4078
Sbjct	4987	CCGTCTGCCAGGACCATCTGGAGTTCTGGGAGAGCGTCTTTACAGGCCTCACCCACATAG	5046
Query	4079	ACGCCCATTCTTGTGCCAGACTAAGCAGGCAGGAGACAACCTCCCCTACCTGGTAGCAT	4138
Sbjct	5047	ACGCCCATTCTTGTGCCAGACTAAGCAGGCAGGAGACAACCTCCCCTACCTGGTAGCAT	5106
Query	4139	ACCAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAATGTGGA	4198
Sbjct	5107	ACCAGGCTACGGTGTGCGCCAGGGCTCAGGCTCCACCTCCATCGTGGGACCAAATGTGGA	5166
Query	4199	AGTGTCTCATAACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCCTGCTGTATAGGCTGG	4258
Sbjct	5167	AGTGTCTCATAACGGCTAAAGCCTACGCTGCACGGGCCAACGCCCCTGCTGTATAGGCTGG	5226
Query	4259	GAGCCGTTCAAACGAGGTTACTACCACACACCCCATAAACAAATACATCATGGCATGCA	4318
Sbjct	5227	GAGCCGTTCAAACGAGGTTACTACCACACACCCCATAAACAAATACATCATGGCATGCA	5286
Query	4319	TGTCGGCTGACCTGGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGCGGAGTCCTAGCAG	4378
Sbjct	5287	TGTCGGCTGACCTGGAGGTGCTCACGAGCACCTGGGTGCTGGTAGGCGGAGTCCTAGCAG	5346
Query	4379	CTCTGGCCGCGTATTGCCTGACAACAGGCAGCGTGGTCATTGTGGGCAGGATCATCTTGT	4438
Sbjct	5347	CTCTGGCCGCGTATTGCCTGACAACAGGCAGCGTGGTCATTGTGGGCAGGATCATCTTGT	5406
Query	4439	CCGGAAAGCCGGCCATCATTCCCGACAGGGAAGTCCTTTACCGGGAGTTTCGATGAGATGG	4498
Sbjct	5407	CCGGAAAGCCGGCCATCATTCCCGACAGGGAAGTCCTTTACCGGGAGTTTCGATGAGATGG	5466
Query	4499	AAGAGTGCGCCTCACACCTCCCTTACATCGAACAGGGAATGCAGCTCGCCGAACAATTCA	4558
Sbjct	5467	AAGAGTGCGCCTCACACCTCCCTTACATCGAACAGGGAATGCAGCTCGCCGAACAATTCA	5526
Query	4559	AACAGAAGGCAATCGGGTTGCTGCAAACAGCCACCAAGCAAGCGGAGGCTGCTGCTCCCG	4618
Sbjct	5527	AACAGAAGGCAATCGGGTTGCTGCAAACAGCCACCAAGCAAGCGGAGGCTGCTGCTCCCG	5586
Query	4619	TGGTGAATCCAAGTGGCGGACCCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTCA	4678

Sbjct	5587	TGGTGAATCCAAGTGGCGGACCCTCGAAGCCTTCTGGGCGAAGCATATGTGGAATTTCA	5646
Query	4679	TCAGCGGGATACAATATTTAGCAGGCTTGCTCCACTCTGCCTGGCAACCCCGCGATAGCAT	4738
Sbjct	5647	TCAGCGGGATACAATATTTAGCAGGCTTGCTCCACTCTGCCTGGCAACCCCGCGATAGCAT	5706
Query	4739	CACTGATGGCATTACAGCCTCTATCACCAGCCCGCTCACCACCCAACATAACCCTCCTGT	4798
Sbjct	5707	CACTGATGGCATTACAGCCTCTATCACCAGCCCGCTCACCACCCAACATAACCCTCCTGT	5766
Query	4799	TTAACATCCTGGGGGGATGGGTGGCCGCCCAACTTGCTCCTCCCAGCGCTGCTTCTGCTT	4858
Sbjct	5767	TTAACATCCTGGGGGGATGGGTGGCCGCCCAACTTGCTCCTCCCAGCGCTGCTTCTGCTT	5826
Query	4859	TCGTAGGCGCCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCTTGGGAAGGTGCTTG	4918
Sbjct	5827	TCGTAGGCGCCGGCATCGCTGGAGCGGCTGTTGGCAGCATAGGCCTTGGGAAGGTGCTTG	5886
Query	4919	TGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTCGTGGCCTTTAAGGTCA	4978
Sbjct	5887	TGGATATTTTGGCAGGTTATGGAGCAGGGGTGGCAGGCGCGCTCGTGGCCTTTAAGGTCA	5946
Query	4979	TGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTACTCCCTGCTATCCTCTCCC	5038
Sbjct	5947	TGAGCGGCGAGATGCCCTCCACCGAGGACCTGGTTAACCTACTCCCTGCTATCCTCTCCC	6006
Query	5039	CTGGCGCCCTAGTCGTCGGGGTCGTGTGCGCAGCGATACTGCGTCGGCACGTGGGCCCAG	5098
Sbjct	6007	CTGGCGCCCTAGTCGTCGGGGTCGTGTGCGCAGCGATACTGCGTCGGCACGTGGGCCCAG	6066
Query	5099	GGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGCTTCGCGGGGTAAACCAG	5158
Sbjct	6067	GGGAGGGGGCTGTGCAGTGGATGAACCGGCTGATAGCGTTTCGCTTCGCGGGGTAAACCAG	6126
Query	5159	TCTCCCCCAGCACTATGTGCCTGAGAGCGACGCTGCAGCACGTGTCACTCAGATCCTCT	5218
Sbjct	6127	TCTCCCCCAGCACTATGTGCCTGAGAGCGACGCTGCAGCACGTGTCACTCAGATCCTCT	6186
Query	5219	CTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCACCAGTGGATCAACGAGGACTGCT	5278
Sbjct	6187	CTAGTCTTACCATCACTCAGCTGCTGAAGAGGCTTCACCAGTGGATCAACGAGGACTGCT	6246
Query	5279	CCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGCACGGTGTTGA	5338
Sbjct	6247	CCACGCCATGCTCCGGCTCGTGGCTAAGAGATGTTTGGGATTGGATATGCACGGTGTTGA	6306
Query	5339	CTGATTTCAAGACCTGGCTCCAGTCCAAGCTCCTGCCGCGATTGCCGGGAGTCCCCTTCT	5398
Sbjct	6307	CTGATTTCAAGACCTGGCTCCAGTCCAAGCTCCTGCCGCGATTGCCGGGAGTCCCCTTCT	6366
Query	5399	TCTCATGTCAACGTGGGTACAAGGGAGTCTGGCGGGGCGACGGCATCATGCAAACCACT	5458
Sbjct	6367	TCTCATGTCAACGTGGGTACAAGGGAGTCTGGCGGGGCGACGGCATCATGCAAACCACT	6426
Query	5459	GCCCATGTGGAGCACAGATACCCGGACATGTGAAAAACGGTTCCATGAGGATCGTGGGGC	5518
Sbjct	6427	GCCCATGTGGAGCACAGATACCCGGACATGTGAAAAACGGTTCCATGAGGATCGTGGGGC	6486
Query	5519	CTAGGACCTGTAGTAACACGTGGCATGGAACATTCCCCATTAACGCGTACACCACGGGCC	5578

Sbjct	6487	CTAGGACCTGTAGTAACACGTGGCATGGAACATTCCCCATTAACGCGTACACCACGGGCC	6546
Query	5579	CCTGCACGCCCTCCCCGGCGCCAAATTATTCTAGGGCGCTGTGGCGGGTGGCTGCTGAGG	5638
Sbjct	6547	CCTGCACGCCCTCCCCGGCGCCAAATTATTCTAGGGCGCTGTGGCGGGTGGCTGCTGAGG	6606
Query	5639	AGTACGTGGAGGTTACGCGGGTGGGGGATTTCCTACTACGTGACGGGCATGACCACTGACA	5698
Sbjct	6607	AGTACGTGGAGGTTACGCGGGTGGGGGATTTCCTACTACGTGACGGGCATGACCACTGACA	6666
Query	5699	ACGTAAAGTGCCCGTGTGAGGTTCCGGCCCCCGAATTCTTCACAGAAGTGGATGGGGTGC	5758
Sbjct	6667	ACGTAAAGTGCCCGTGTGAGGTTCCGGCCCCCGAATTCTTCACAGAAGTGGATGGGGTGC	6726
Query	5759	GGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCCTACGGGAGGAGGTACATTCTCTGG	5818
Sbjct	6727	GGTTGCACAGGTACGCTCCAGCGTGCAAACCCCTCCTACGGGAGGAGGTACATTCTCTGG	6786
Query	5819	TCGGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATGCGAGCCCGAACCGGACGTAG	5878
Sbjct	6787	TCGGGCTCAATCAATACCTGGTTGGGTACAGCTCCCATGCGAGCCCGAACCGGACGTAG	6846
Query	5879	CAGTGCTCACTTCCATGCTCACCGACCCCTCCACATTACGGCGGAGACGGCTAAGCGTA	5938
Sbjct	6847	CAGTGCTCACTTCCATGCTCACCGACCCCTCCACATTACGGCGGAGACGGCTAAGCGTA	6906
Query	5939	GGCTGGCCAGGGGATCTCCCCCTCCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGC	5998
Sbjct	6907	GGCTGGCCAGGGGATCTCCCCCTCCTTGGCCAGCTCATCAGCTAGCCAGCTGTCTGCGC	6966
Query	5999	CTTCCTTGAAGGCAACATGCACTACCCGTCATGACTCCCCGGACGCTGACCTCATCGAGG	6058
Sbjct	6967	CTTCCTTGAAGGCAACATGCACTACCCGTCATGACTCCCCGGACGCTGACCTCATCGAGG	7026
Query	6059	CCAACCTCCTGTGGCGGCAGGAGATGGGCGGGAACATCACCCGCGTGGAGTCAGAAAATA	6118
Sbjct	7027	CCAACCTCCTGTGGCGGCAGGAGATGGGCGGGAACATCACCCGCGTGGAGTCAGAAAATA	7086
Query	6119	AGGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCAAGCGGAGGAGGATGAGAGGGAAGTAT	6178
Sbjct	7087	AGGTAGTAATTTTGGACTCTTTTCGAGCCGCTCCAAGCGGAGGAGGATGAGAGGGAAGTAT	7146
Query	6179	CCGTTCCGGCGGAGATCCTGCGGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGG	6238
Sbjct	7147	CCGTTCCGGCGGAGATCCTGCGGAGGTCCAGGAAATTCCTCGAGCGATGCCCATATGGG	7206
Query	6239	CACGCCCCGATTACAACCCTCCACTGTTAGAGTCCTGGAAGGACCCGGACTACGTCCCTC	6298
Sbjct	7207	CACGCCCCGATTACAACCCTCCACTGTTAGAGTCCTGGAAGGACCCGGACTACGTCCCTC	7266
Query	6299	CAGTGGTACACGGGTGTCCATTGCCGCTGCCAAGGCCCTCCGATACCACCTCCACGGA	6358
Sbjct	7267	CAGTGGTACACGGGTGTCCATTGCCGCTGCCAAGGCCCTCCGATACCACCTCCACGGA	7326
Query	6359	GGAAGAGGACGGTTGTCTGTGAGAATCTACCGTGTCTTCTGCCTTGGCGGAGCTCGCCA	6418
Sbjct	7327	GGAAGAGGACGGTTGTCTGTGAGAATCTACCGTGTCTTCTGCCTTGGCGGAGCTCGCCA	7386
Query	6419	CAAAGACCTTCGGCAGCTCCGAATCGTCGGCCGTCGACAGCGGCACGGCAACGGCCTCTC	6478

Sbjct	7387	CAAAGACCTTCGGCAGCTCCGAATCGTCGGCCGTCGACAGCGGCACGGCAACGGCCTCTC	7446
Query	6479	CTGACCAGCCCTCCGACGACGGCGACGCGGGATCCGACGTTGAGTCGTA	6538
Sbjct	7447	CTGACCAGCCCTCCGACGACGGCGACGCGGGATCCGACGTTGAGTCGTA	7506
Query	6539	CCCCCTTGAGGGGGAGCCGGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAA	6598
Sbjct	7507	CCCCCTTGAGGGGGAGCCGGGGGATCCCGATCTCAGCGACGGGTCTTGGTCTACCGTAA	7566
Query	6599	GCGAGGAGGCTAGTGAGGACGTCGTCTGCTGCTCGATGTCCTACACATGGACAGGCGCCC	6658
Sbjct	7567	GCGAGGAGGCTAGTGAGGACGTCGTCTGCTGCTCGATGTCCTACACATGGACAGGCGCCC	7626
Query	6659	TGATCACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGAGCAACTCTT	6718
Sbjct	7627	TGATCACGCCATGCGCTGCGGAGGAAACCAAGCTGCCCATCAATGCACTGAGCAACTCTT	7686
Query	6719	TGCTCCGTCAACACAACCTTGGTCTATGCTACAACATCTCGCAGCGCAAGCCTGCGGCAGA	6778
Sbjct	7687	TGCTCCGTCAACACAACCTTGGTCTATGCTACAACATCTCGCAGCGCAAGCCTGCGGCAGA	7746
Query	6779	AGAAGGTCACCTTTGACAGACTGCAGGTCTGGACGACCACTACCGGGACGTGCTCAAGG	6838
Sbjct	7747	AGAAGGTCACCTTTGACAGACTGCAGGTCTGGACGACCACTACCGGGACGTGCTCAAGG	7806
Query	6839	AGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAGGAAGCCTGTA	6898
Sbjct	7807	AGATGAAGGCGAAGGCGTCCACAGTTAAGGCTAAACTTCTATCCGTGGAGGAAGCCTGTA	7866
Query	6899	AGCTGACGCCCCACATTTCGGCCAGATCTAAATTTGGCTATGGGGCAAAGGACGTCCGGA	6958
Sbjct	7867	AGCTGACGCCCCACATTTCGGCCAGATCTAAATTTGGCTATGGGGCAAAGGACGTCCGGA	7926
Query	6959	ACCTATCCAGCAAGGCCGTTAACCACATCCGCTCCGTGTGGAAGGACTTGCTGGAAGACA	7018
Sbjct	7927	ACCTATCCAGCAAGGCCGTTAACCACATCCGCTCCGTGTGGAAGGACTTGCTGGAAGACA	7986
Query	7019	CTGAGACACCAATTGACACCACCATCATGGCAAAAAATGAGGTTTTCTGCGTCCAACCAG	7078
Sbjct	7987	CTGAGACACCAATTGACACCACCATCATGGCAAAAAATGAGGTTTTCTGCGTCCAACCAG	8046
Query	7079	AGAAGGGGGGCGCAAGCCAGCTCGCCTTATCGTATTCCCAGATTTGGGGGTTTCGTGTGT	7138
Sbjct	8047	AGAAGGGGGGCGCAAGCCAGCTCGCCTTATCGTATTCCCAGATTTGGGGGTTTCGTGTGT	8106
Query	7139	GCGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCTCCCTCAGGCCGTGATGGGCTCTT	7198
Sbjct	8107	GCGAGAAAATGGCCCTTTACGATGTGGTCTCCACCCTCCCTCAGGCCGTGATGGGCTCTT	8166
Query	7199	CATACGGATTCCAATACTCTCCTGGACAGCGGGTCGAGTTCCTGGTGAATGCCTGGAAAG	7258
Sbjct	8167	CATACGGATTCCAATACTCTCCTGGACAGCGGGTCGAGTTCCTGGTGAATGCCTGGAAAG	8226
Query	7259	CGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTTGACTCAACGGTCACTG	7318
Sbjct	8227	CGAAGAAATGCCCTATGGGCTTCGCATATGACACCCGCTGTTTTGACTCAACGGTCACTG	8286
Query	7319	AGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCGAAGCCA	7378

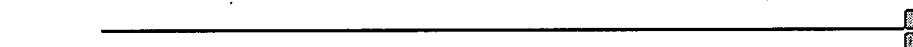
Sbjct	8287	AGAATGACATCCGTGTTGAGGAGTCAATCTACCAATGTTGTGACTTGGCCCCCGAAGCCA	8346
Query	7379	GACAGGCCATAAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTAATTCTA	7438
Sbjct	8347	GACAGGCCATAAGGTCGCTCACAGAGCGGCTTTACATCGGGGGCCCCCTGACTAATTCTA	8406
Query	7439	AAGGGCAGAACTGCGGCTATCGCCGGTGCCGCGGAGCGGTGTACTGACGACCAGCTGCG	7498
Sbjct	8407	AAGGGCAGAACTGCGGCTATCGCCGGTGCCGCGGAGCGGTGTACTGACGACCAGCTGCG	8466
Query	7499	GTAATACCCTCACATGTTACTTGAAGGCCGCTGCGGCCTGTGCGAGCTGCGAAGCTCCAGG	7558
Sbjct	8467	GTAATACCCTCACATGTTACTTGAAGGCCGCTGCGGCCTGTGCGAGCTGCGAAGCTCCAGG	8526
Query	7559	ACTGCACGATGCTCGTATGCGGAGACGACCTTGTCGTTATCTGTGAAAGCGCGGGGACCC	7618
Sbjct	8527	ACTGCACGATGCTCGTATGCGGAGACGACCTTGTCGTTATCTGTGAAAGCGCGGGGACCC	8586
Query	7619	AAGAGGACGAGGCGAGCCTACGGGCCTTCACGGAGGCTATGACTAGATACTCTGCCCCCC	7678
Sbjct	8587	AAGAGGACGAGGCGAGCCTACGGGCCTTCACGGAGGCTATGACTAGATACTCTGCCCCCC	8646
Query	7679	CTGGGGACCCGCCCAAACCAGAATACGACTTGGAGTTGATAACATCATGCTCCTCCAATG	7738
Sbjct	8647	CTGGGGACCCGCCCAAACCAGAATACGACTTGGAGTTGATAACATCATGCTCCTCCAATG	8706
Query	7739	TGTCAGTCGCGCACGATGCATCTGGCAAAGGGTGTACTATCTCACCCGTGACCCACCA	7798
Sbjct	8707	TGTCAGTCGCGCACGATGCATCTGGCAAAGGGTGTACTATCTCACCCGTGACCCACCA	8766
Query	7799	CCCCCTTGCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAG	7858
Sbjct	8767	CCCCCTTGCGCGGGCTGCGTGGGAGACAGCTAGACACACTCCAGTCAATTCCTGGCTAG	8826
Query	7859	GCAACATCATCATGTATGCGCCACCTTGTTGGGAAGGATGATCCTGATGACTCATTCT	7918
Sbjct	8827	GCAACATCATCATGTATGCGCCACCTTGTTGGGAAGGATGATCCTGATGACTCATTCT	8886
Query	7919	TCTCCATCCTTCTAGCTCAGGAACAACCTGAAAAAGCCCTAGATTGTCAGATCTACGGGG	7978
Sbjct	8887	TCTCCATCCTTCTAGCTCAGGAACAACCTGAAAAAGCCCTAGATTGTCAGATCTACGGGG	8946
Query	7979	CCTGTTACTCCATTGAGCCACTTGACCTACCTCAGATCATTCAACGACTCCATGGCCTTA	8038
Sbjct	8947	CCTGTTACTCCATTGAGCCACTTGACCTACCTCAGATCATTCAACGACTCCATGGCCTTA	9006
Query	8039	GCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCCTCA	8098
Sbjct	9007	GCGCATTTTCACTCCATAGTTACTCTCCAGGTGAGATCAATAGGGTGGCTTCATGCCTCA	9066
Query	8099	GGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAAGTGTCCGCGCTA	8158
Sbjct	9067	GGAAACTTGGGGTACCGCCCTTGCGAGTCTGGAGACATCGGGCCAGAAGTGTCCGCGCTA	9126
Query	8159	GGCTACTGTCCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTCAACTGGGCAG	8218
Sbjct	9127	GGCTACTGTCCCAGGGGGGAGGGCTGCCACTTGTGGCAAGTACCTCTTCAACTGGGCAG	9186
Query	8219	TAAGGACCAAGCTCAAACCTCACTCCAATCCCGGCTGCGTCCCAGTTGGATTTATCCAGCT	8278

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Sbjct  9187  TAAGGACCAAGCTCAAACCTCACTCCAATCCCGGCTGCGTCCCAGTTGGATTTATCCAGCT  9246
Query  8279  GGTTCGTTGCTGGTTACAGCGGGGAGACATATATCACAGCCTGTCTCGTGCCCGACCCC  8338
          |||
Sbjct  9247  GGTTCGTTGCTGGTTACAGCGGGGAGACATATATCACAGCCTGTCTCGTGCCCGACCCC  9306
Query  8339  GCTGGTTCATGTGGTGCCTACTCCTACTTTCTGTAGGGGTAGGCATCTATCTACTCCCCA  8398
          |||
Sbjct  9307  GCTGGTTCATGTGGTGCCTACTCCTACTTTCTGTAGGGGTAGGCATCTATCTACTCCCCA  9366
Query  8399  ACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTG  8444
          |||
Sbjct  9367  ACCGATGAACGGGGAGCTAAACACTCCAGGCCAATAGGCCATCCTG  9412
```



Score = 696 bits (362), Expect = 0.0
Identities = 376/376 (100%), Gaps = 0/376 (0%)
Strand=Plus/Plus

```
Query  2      CCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCCTGTGAGGAACTACTGT  61
          |||
Sbjct  2      CCAGCCCCCGATTGGGGGCGACACTCCACCATAGATCACTCCCCTGTGAGGAACTACTGT  61
Query  62      CTTACAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCTCCAGGACC  121
          |||
Sbjct  62      CTTACAGCAGAAAGCGTCTAGCCATGGCGTTAGTATGAGTGTCTGTCAGCCTCCAGGACC  121
Query  122     CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG  181
          |||
Sbjct  122     CCCCCTCCCGGGAGAGCCATAGTGGTCTGCGGAACCGGTGAGTACACCGGAATTGCCAGG  181
Query  182     ACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCG  241
          |||
Sbjct  182     ACGACCGGGTCCTTTCTTGGATCAACCCGCTCAATGCCTGGAGATTTGGGCGTGCCCCCG  241
Query  242     CGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGGCCTTGTGGTACTGCCTGATAGGG  301
          |||
Sbjct  242     CGAGACTGCTAGCCGAGTAGTGTGGGTGCGGAAAGGCCTTGTGGTACTGCCTGATAGGG  301
Query  302     TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACC  361
          |||
Sbjct  302     TGCTTGCGAGTGCCCCGGGAGGTCTCGTAGACCGTGCACCATGAGCACGAATCCTAAACC  361
Query  362     TCAAAGAAAAACCAA  377
          |||
Sbjct  362     TCAAAGAAAAACCAA  377
```



Score = 189 bits (98), Expect = 2e-43
Identities = 98/98 (100%), Gaps = 0/98 (0%)

Strand=Plus/Plus

```
Query  8540  GGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAAGGTCCGTGAGCCGCTTGACT  8599
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  9508  GGTGGCTCCATCTTAGCCCTAGTCACGGCTAGCTGTGAAAGGTCCGTGAGCCGCTTGACT  9567

Query  8600  GCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCAAGT  8637
          ||||||||||||||||||||||||||||||||
Sbjct  9568  GCAGAGAGTGCTGATACTGGCCTCTCTGCAGATCAAGT  9605
```

CPU time: 0.12 user secs. 0.04 sys. secs 0.16 total secs.